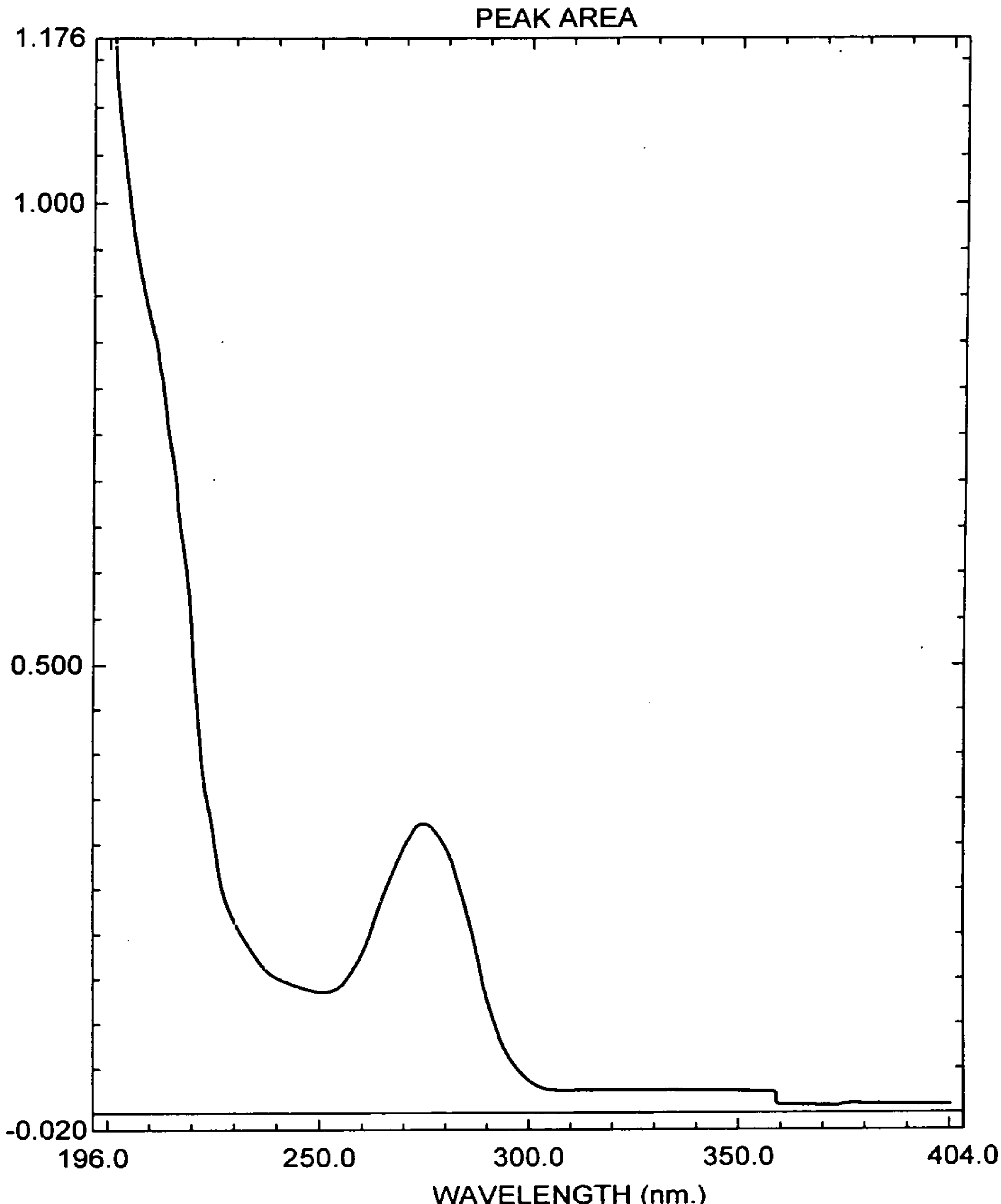
09/881,569
U 013488-3



FILE NAME: SY-12

CREATED: 14:29 01-01-22
DATA: ORIGINAL

MEASURING MODE: ABS.
SCAN SPEED: FAST
SLIT WIDTH: 1.0
SAMPLING INTERVAL: 0.2

RESULT - (AREA-FACTOR) DIVISOR FACTOR = 9.999

REGIUM START END DIVISOR AREA RESULT

FIG. 1

C A M A G **ILC** Evaluation Software
****

ARBRO PHARMACEUTICALS LTD 6/14 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI
PHONE: 5467228.515-0437. FAX: 91-11-5463784, E-mail: arbo@vsn1.com

TLC/HPTLC-Integration (CATS3.18 S/N:0207A004 / SCANNER I I V3.14 S/N:990602)

ESTIMATION OF L-LYSINE BY HPTLC

Calibr. Table	Calibration Table created:	ARBRO PHARMA LTD	
	File name: AMINO	3/JUN/ 0	14:49:46
Scan	User name wnile measuring :	ARBRO PHARMA LTD	
	File name: AMINO	3/JUN/ 0	14:54:52
INTEGRATION	User while integrating:	ARBRO PHARMA LTD	
	File name: AMINO	3/JUN/ 0	15:19:26

Track 1. Analysis a:

Peak	start		max			end		area	
#	mm	h	mm	h	[%]	mm	h	a	[%]
1	61.1	0.4	72.6	64.1	100.00	78.2	0.1	3186.2	100.00

Total height = 64.1 Total area = 3186.2

Track 2. Standard level 1:

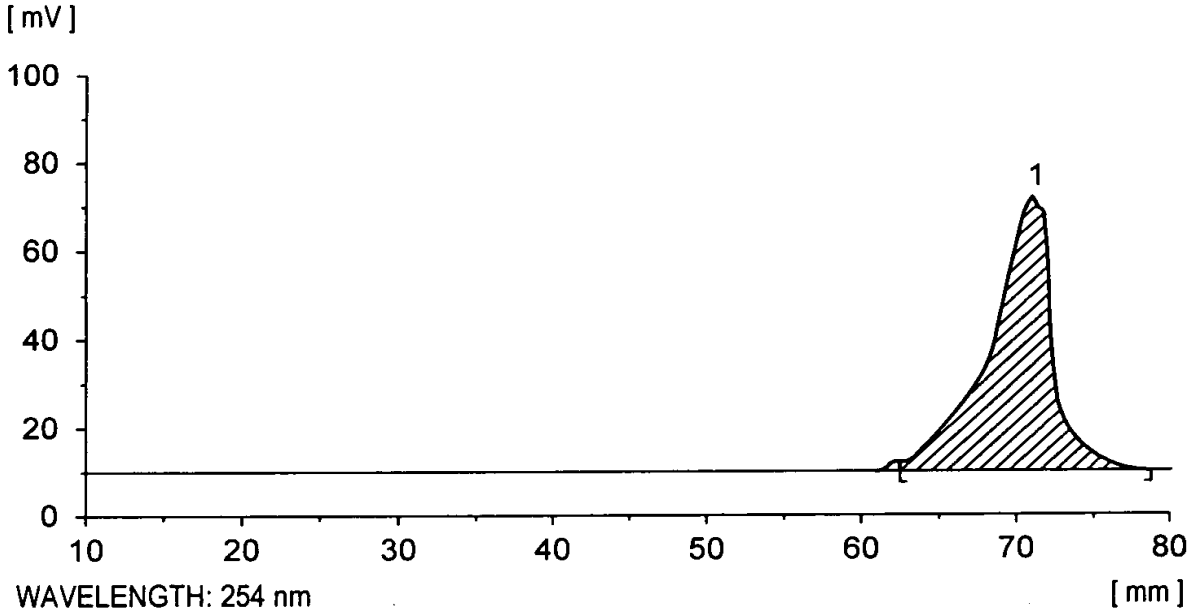
Peak	start		max			end		area	
#	mm	h	mm	h	[%]	mm	h	a	[%]
1	62.9	2.8	71.0	63.5	100.00	78.8	0.0	3133.9	100.00

Total height = 63.5 Total area = 3133.9

F I G. 2A

CALIBRATION : H : AMINO ARBRO PHARMA LTD 3/JUN/2000 15:05
METHOD SCAN INTEGRATION CALIBRATION DATA END HELP

STANDARD LEVEL 1



TRACK: 2, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

TRACK 2. STANDARD LEVEL 1

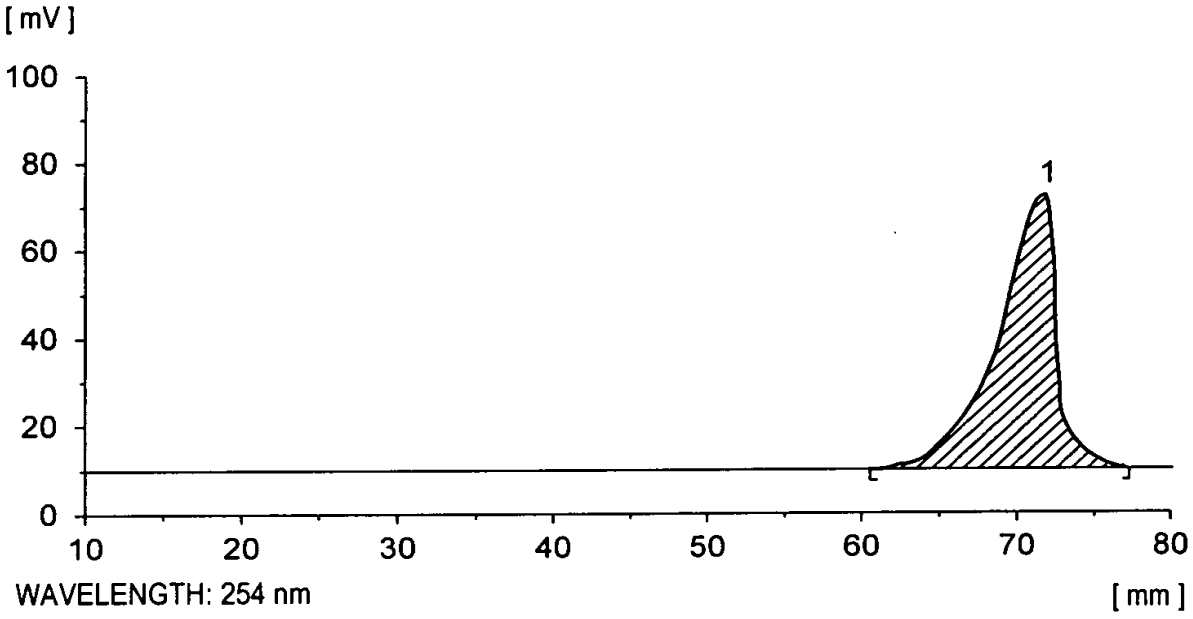
PEAK	START		MAX			END		AREA	
#	mm	h	mm	h	[%]	mm	h	a	[%]
1	62.9	2.8	71.0	63.5	100.00	78.8	0.0	3133.9	100.00

TOTAL HEIGHT = 63.5 TOTAL AREA = 3133.9

FIG. 2b

CALIBRATION : H : AMINO ARBRO PHARMA LTD 3/JUN/2000 15:10
METHOD SCAN [INTEGRATION] CALIBRATION DATA END HELP

STANDARD LEVEL 1



TRACK: 1, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

TRACK 1. ANALYSIS a:

PEAK	START		MAX			END		AREA	
#	mm	h	mm	h	[%]	mm	h	a	[%]
1	61.1	0.4	72.6	64.1	100.00	78.2	01	3186.2	100.00

TOTAL HEIGHT = 64.1 TOTAL AREA = 3186.2

FIG. 2c

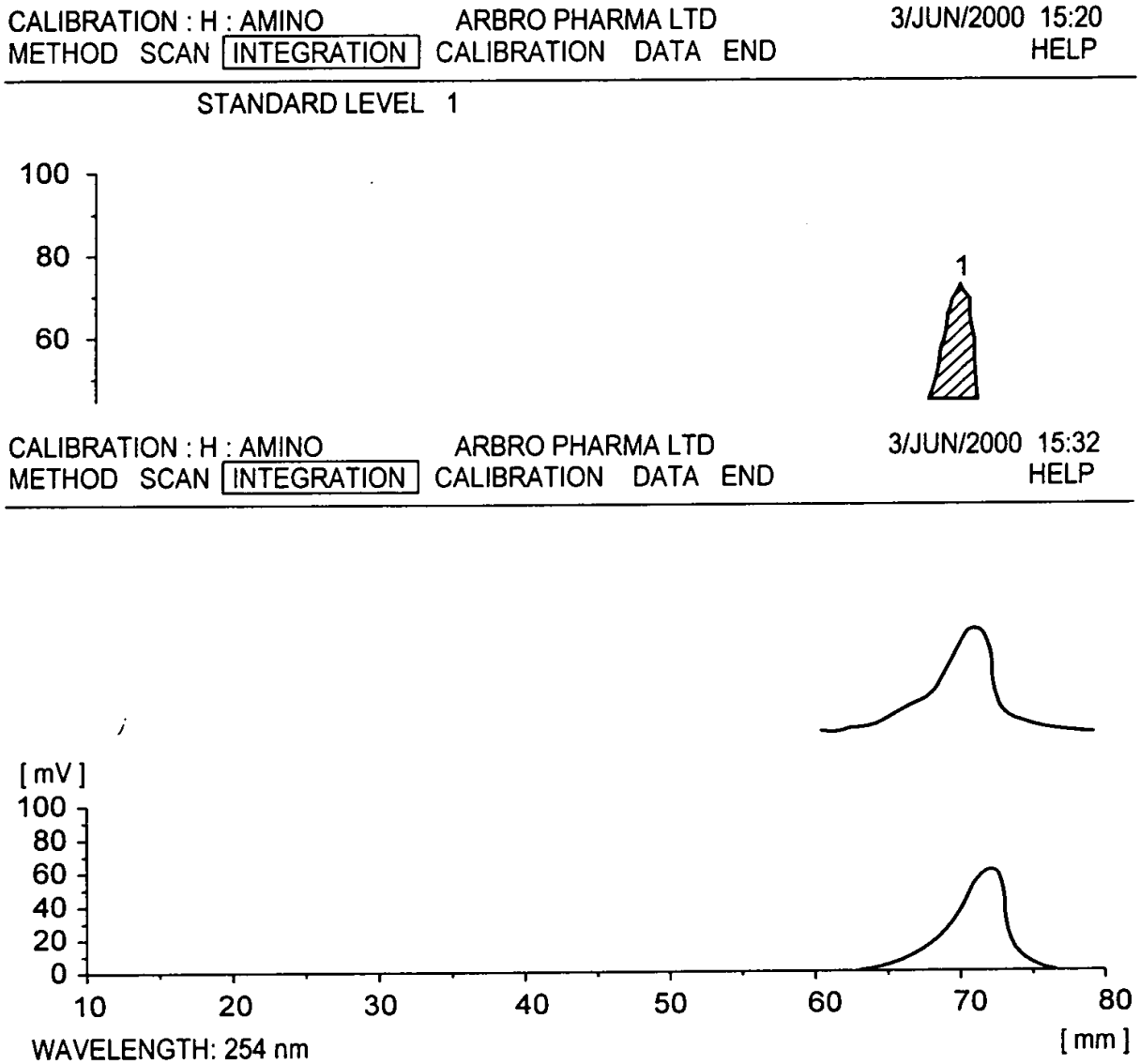


FIG. 2d

SUBMITTER: PUSHPA KHANNA

SAMPLE NAME: GOURDIN DATE:

SEQUENCE:	ASP GLY	LEU VAL ILE	SER GLU	GLN GLU	GLN THR	TYR VAL THR	GLY	SER GLN THR	HIS ARG GLN LEU
CYCLE #:	1	2	3	4	5	6	7	8	9

SEQUENCE:	LYS ARG	TYR ILE LEU	ARG HIS ALA LYS	HIS GLU TYR	ASN ASP	ARG MET ILE	GLY ASP ASN LEU	ARG THR ASP	ARG HIS ALA
CYCLE #:	10	11	12	13	14	15	16	17	18

SEQUENCE:	SER GLU LEU LYS	ARG GLU	SER PRO ALA	ILE ASP	GLU LEU ILE	PHE TYR	THR SER ASN	PRO ARG ALA HIS	HIS ARG GLY
CYCLE #:	19	20	21	22	23	24	25	26	27

SEQUENCE:	GLY VAL ALA	GLY	ARG	VAL LEU ILE	ASN SER	PRO ILE THR	ALA VAL	ASN
CYCLE #:	28	29	30	31	32	33	34	35

YIELD(pmol): ILE(2) 98.11 YIELD(pmol): GLU(3) 56.13

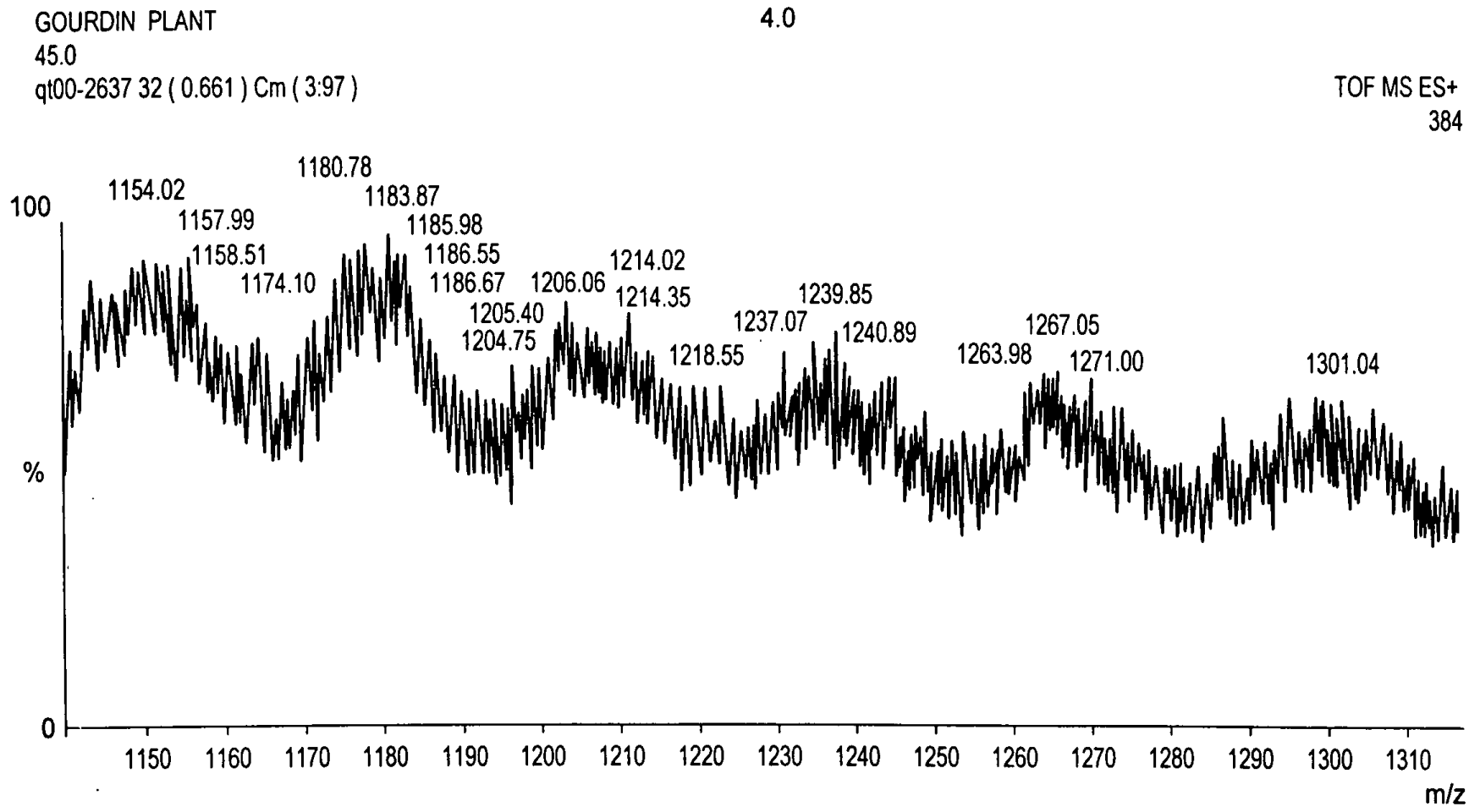
CARRYOVER: ILE(6) 22.6% REP YIELD: ILE(2.23) 92.3%

SEQSTD YIELD: NL(6) 2.30 SEQSTD CARRYOVER: NL(6) 23.0%

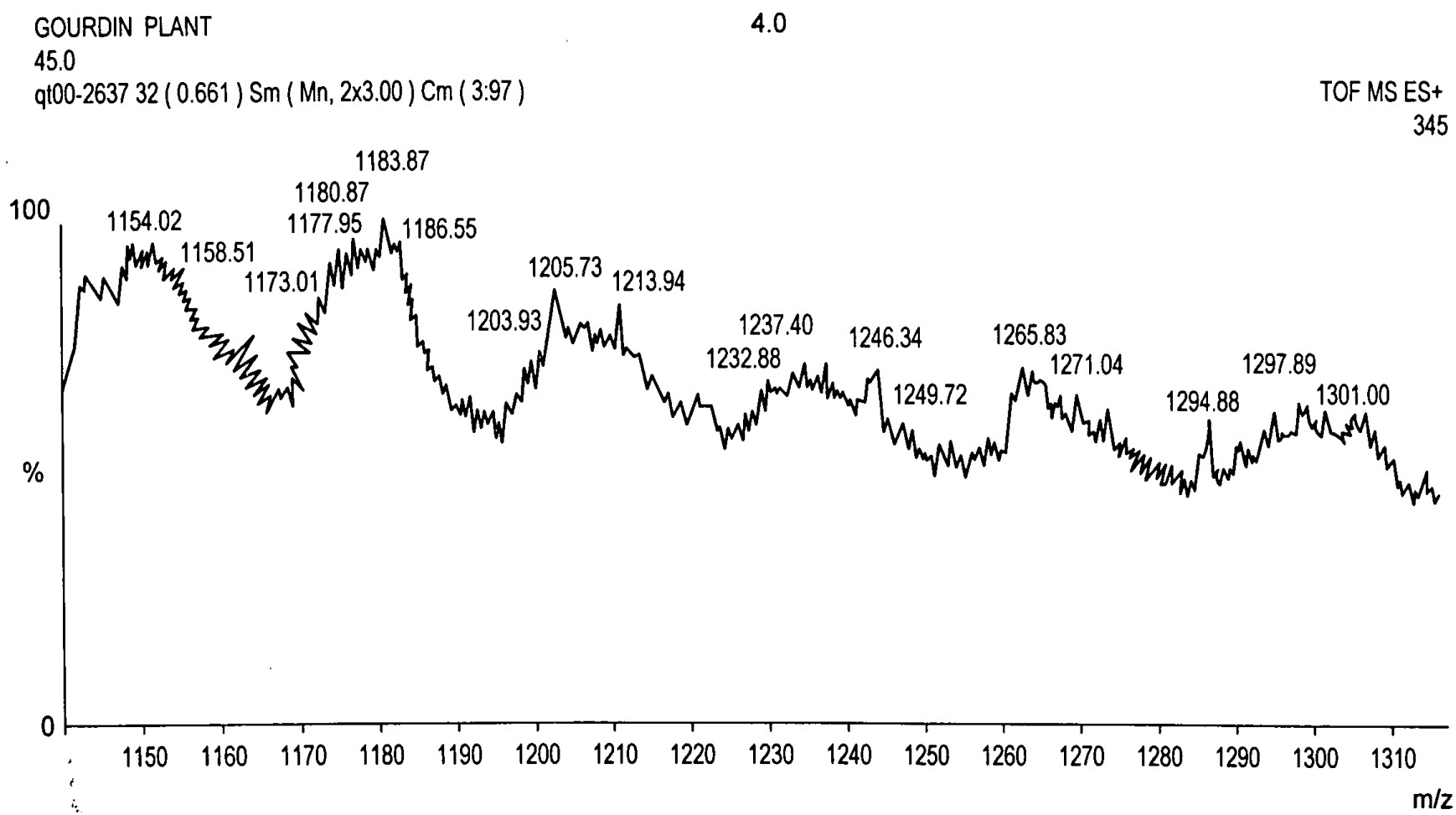
SEQSTD REP YIELD: NL(6.11) 97.0%

COMMENTS: Mixtures with interchangeable amino acid at positions 12,13,15-19, 25-27 and 31-34. Appears to be a mixture of sequences.

FIG. 3a



F I G. 4a1



F I G. 4a2

GOURDIN PLANT
45.0
qt00-2637 32 (0.661) Cm (3:97)

4.0

TOF MS ES+
555

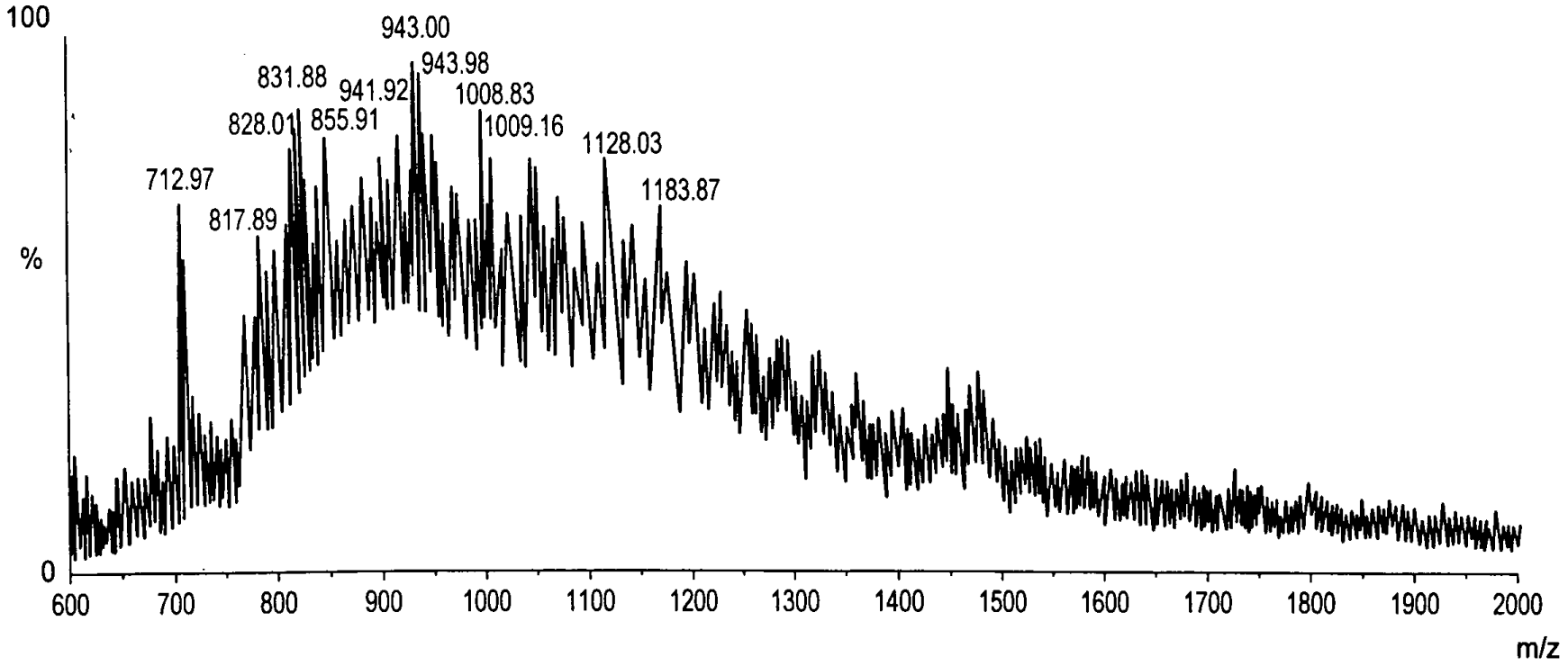
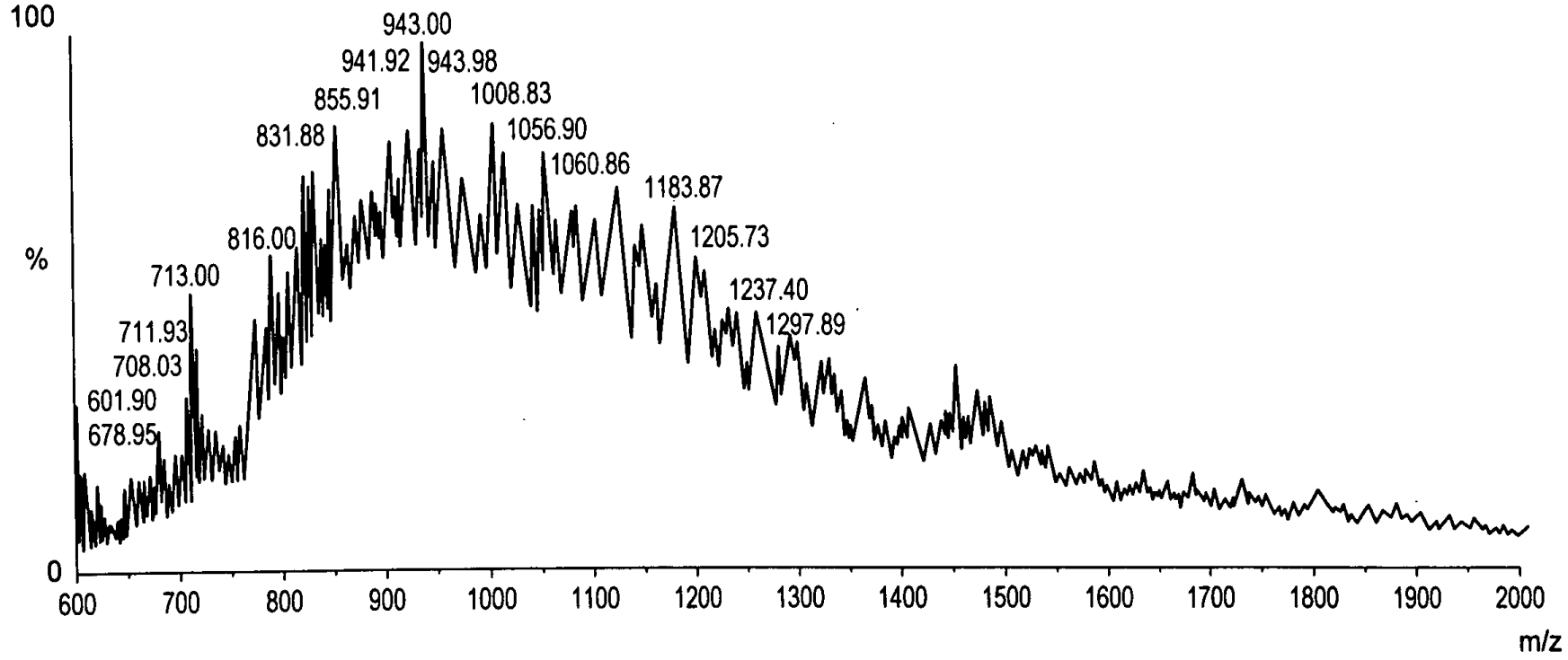


FIG. 4b1

GOURDIN PLANT
45.0
qt00-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)

4.0

TOF MS ES+
501



F I G. 4b2

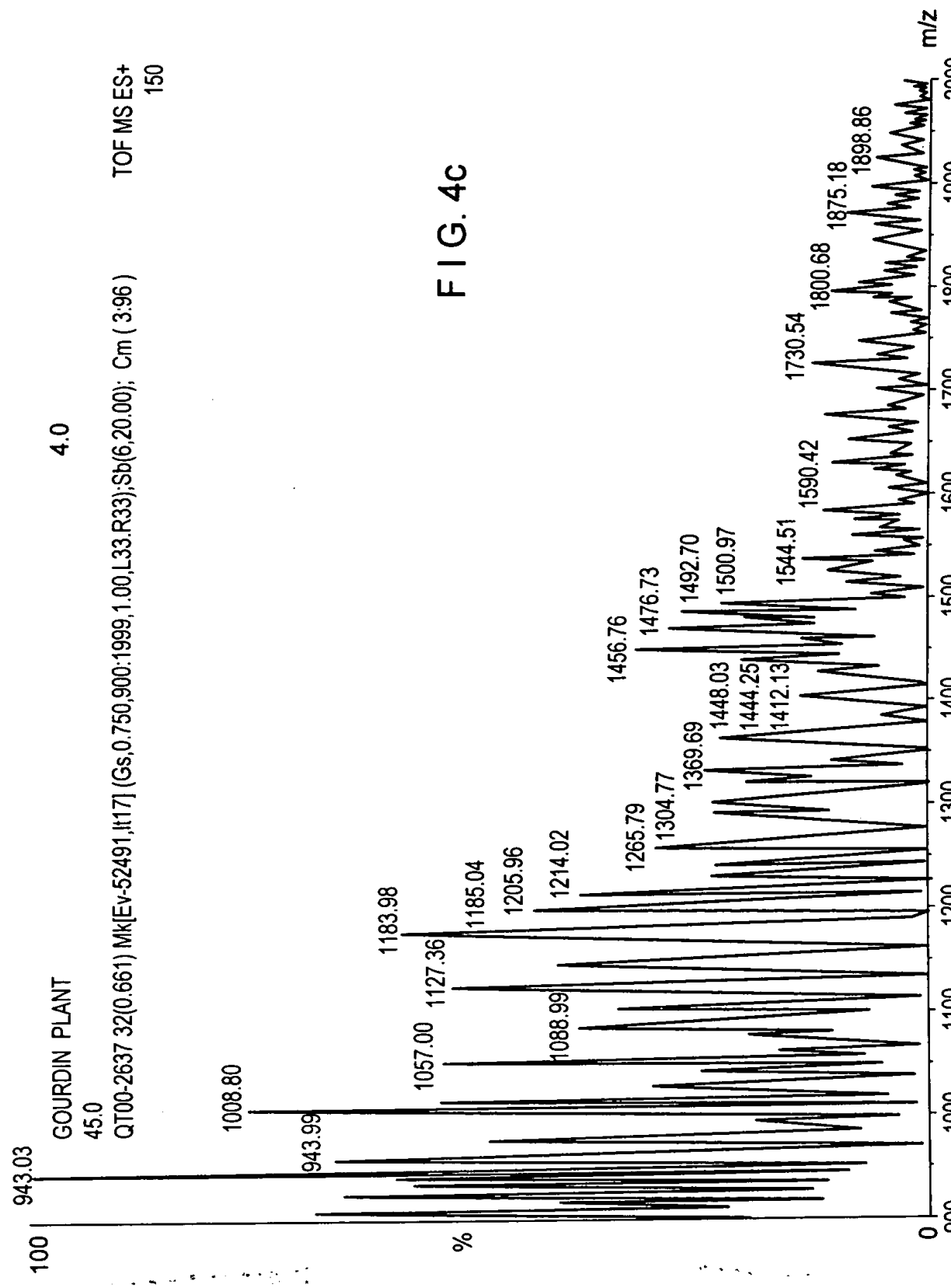


FIG. 4c

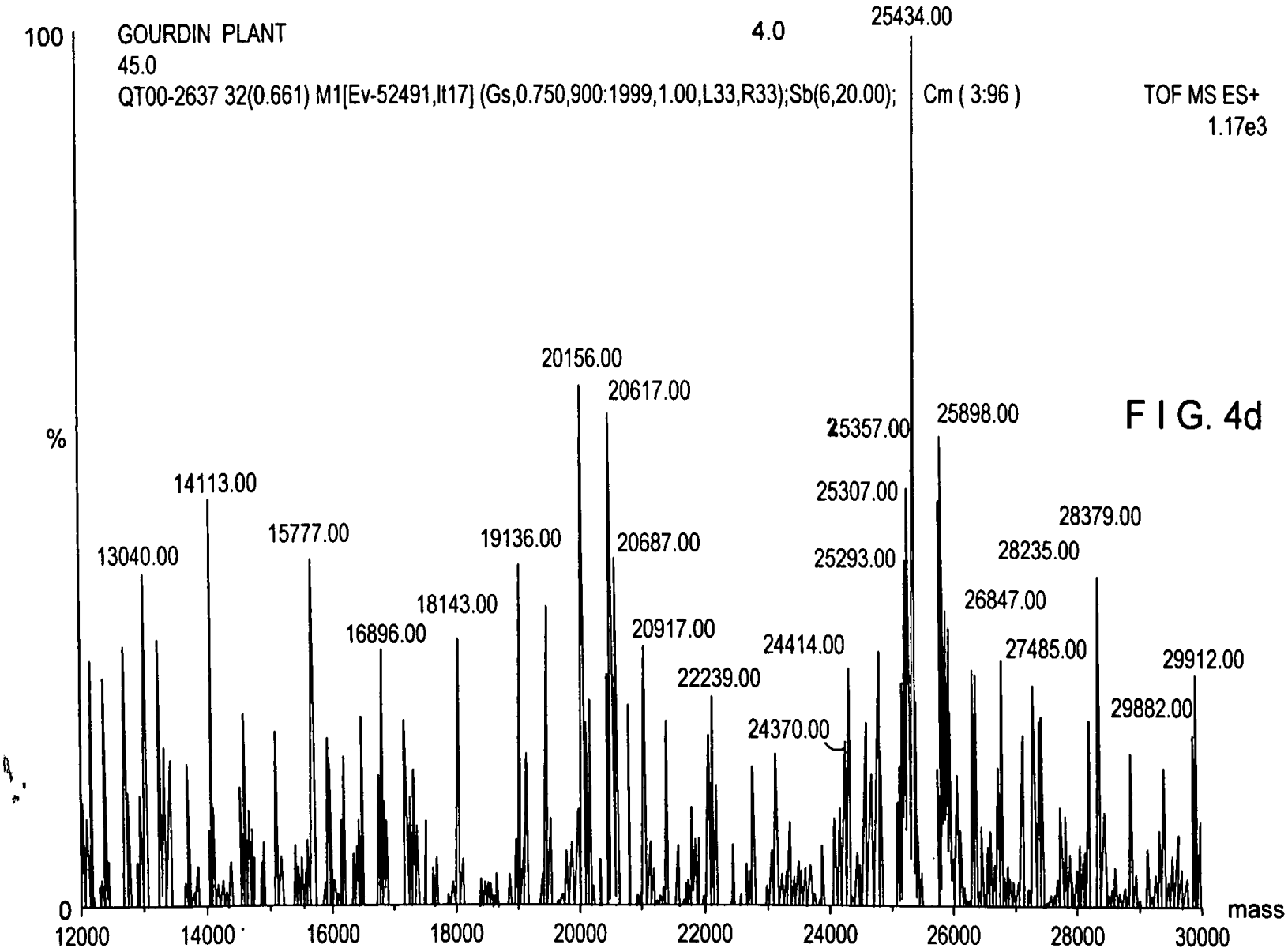


FIG. 4d

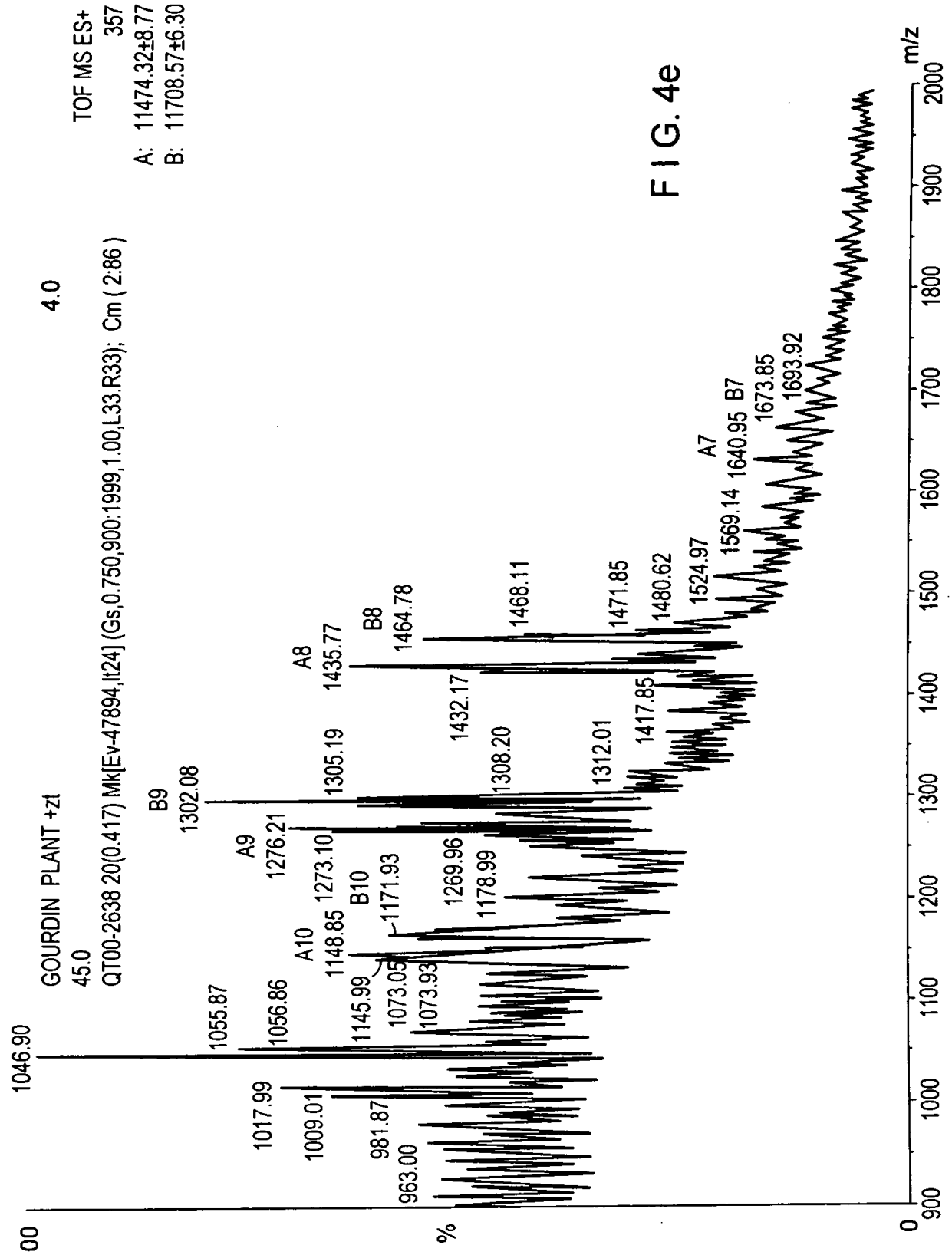
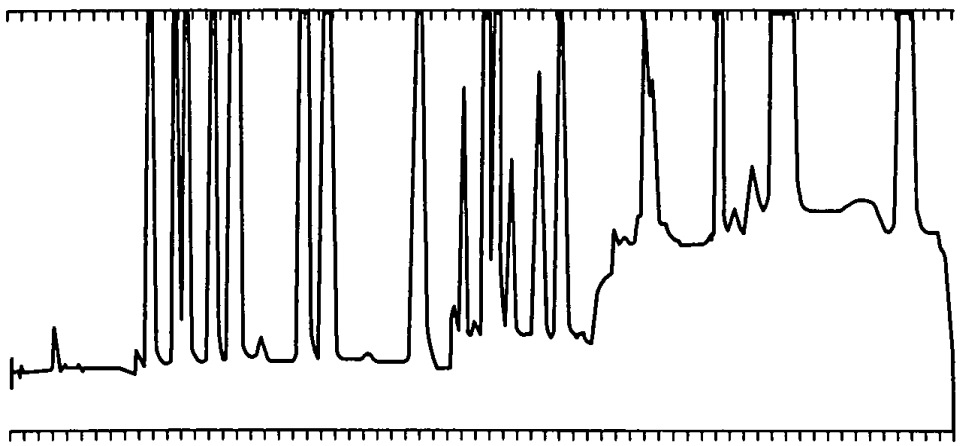


FIG. 4e



INTERFACE 01 0-68 Min SCALE: 15 Mv Ch. A, 15 Mv Ch. B
AMINO ACID ANALYSI PROCESSED: 11-22-2000 14:26:30, SEGMENT 17, CYCLE 936
RAW DATA SAVED IN FILE K : AAA936.PTS SECOND CHANNEL STORED IN K : BAA936.PTS

EXTERNAL STANDARD TABLE

********** 11-22-2000 14 : 26 : 30 Version 4.1 **********

Sample Name: amino acid analysis Data File: K:AAA936

Date: 11-22-2000 14 : 26 : 30 Method: F:REBECKA 11-22-2000 13 : 54 : 21 # 457

Interface: 0 Cycle #: 936 Operator jmc Channel #: 0 Vial #: N.A.

Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

****

Starting Delay:	0.00	Ending retention time:	68.00
Area reject:	5000	One sample per:	2.002 sec.
Amount injected:	1.00	Dilution factor:	1.00
Sample weight:	1.000000		

SEE FIG. 5a2

FIG. 5a1

SEE FIG. 5a1

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/ AREA
1	2.936			0.1504%	20695	1550	13.4	1	6	-1.592	3.4373E-06
2	8.609			0.0856%	9566	096	13.7	1	6	0	4.28185-06
3	9.543	asx	3.6346	7.6853%	1019304	61489	16.6	1	6	.5811	3.5658E-06
4	11.378	thr	1.1549	2.4420%	314916	15245	20.7	2	6	.1132	3.6674E-06
5	12.112	ser	2.0456	4.3254%	595007	27668	21.5	2	6	0	3.4380E-06
6	14.081	int. std.	1.0397	2.1985%	576309	23599	24.4	2	6	0	1.0041E-06
7	15.649	glx	6.6195	13.9567%	1959672	71617	27.4	2	6	.1667	3.3779E-06
8	17.651	pro+ cys	2.1133	6.1414%	28161	809	34.8	2	6	-.2854	1.0314E-04
9	20.554	gly	3.4509	7.2968%	1098728	36599	30.0	2	9	0	3.1408E-06
10	22.256	ala	2.8168	5.9961%	801412	25276	31.7	2	9	0	3.5248E-06
11	28.996	val	2.6160	5.4358%	783543	16490	42.7	1	9	0	3.6541E-06
12	32.299	set	0.5625	1.1894%	157161	8772	17.9	1	16	.0101	3.5792E-06
13	33.166		0.0000	0.0000%	10132	523	19.4	1			0.0000E+00
14	33.967	ileu	1.8404	3.8914%	535119	23330	22.9	2	16	-.0931	3.4392E-06
15	34.735	leu	3.1701	6.7031%	953284	38035	25.1	2	16	0	3.3255E-06
16	35.902	nl-std.	6.2739	0.5791%	163238	6196	26.3	2	16	0	1.6777E-06
17	37.871	tyr	1.0645	2.2508%	290327	9412	30.8	1	16	0	3.6666E-06
18	39.473	phe	1.6115	3.4075%	408260	12881	31.7	1	16	0	3.9472E-06
19	45.479	his	1.2110	2.6711%	203562	8185	24.9	2	16	0	
20	46.013		0.0000	0.0000%	154147	5442	26.3	2			0.0000E+00
21	50.751	lys	1.2451	2.6327%	385456	13267	29.1	2	16	0	3.2302E-06
22	51.885			0.3929%	32441	913	35.5	2	16	0	5.7275E-06
23	53.287		0.0000	0.0000%	102408	2246	46.6	2			0.0000E+00
24	55.355	NH4	6.1666	13.0391%	3568874	61870	57.7	2	16	0	1.7279E-06
25	64.197	arg	3.5602	7.5279%	1016938	22156	45.9	1	16	0	3.5009E-06
	TOTAL AMOUNT:		47.2934								

FIG. 5a2

AREAS, TIMES, AND HEIGHTS STORED IN : K: AAA936.ATB
DATA FILE = K: AAA936.PTS PRINTED ON 11-22-2000 AT 14:27:06
START TIME : 0.00 min. STOP TIME : 68.00 min. OFFSET : 0 mv
FULL RANGE : 15 millivolts

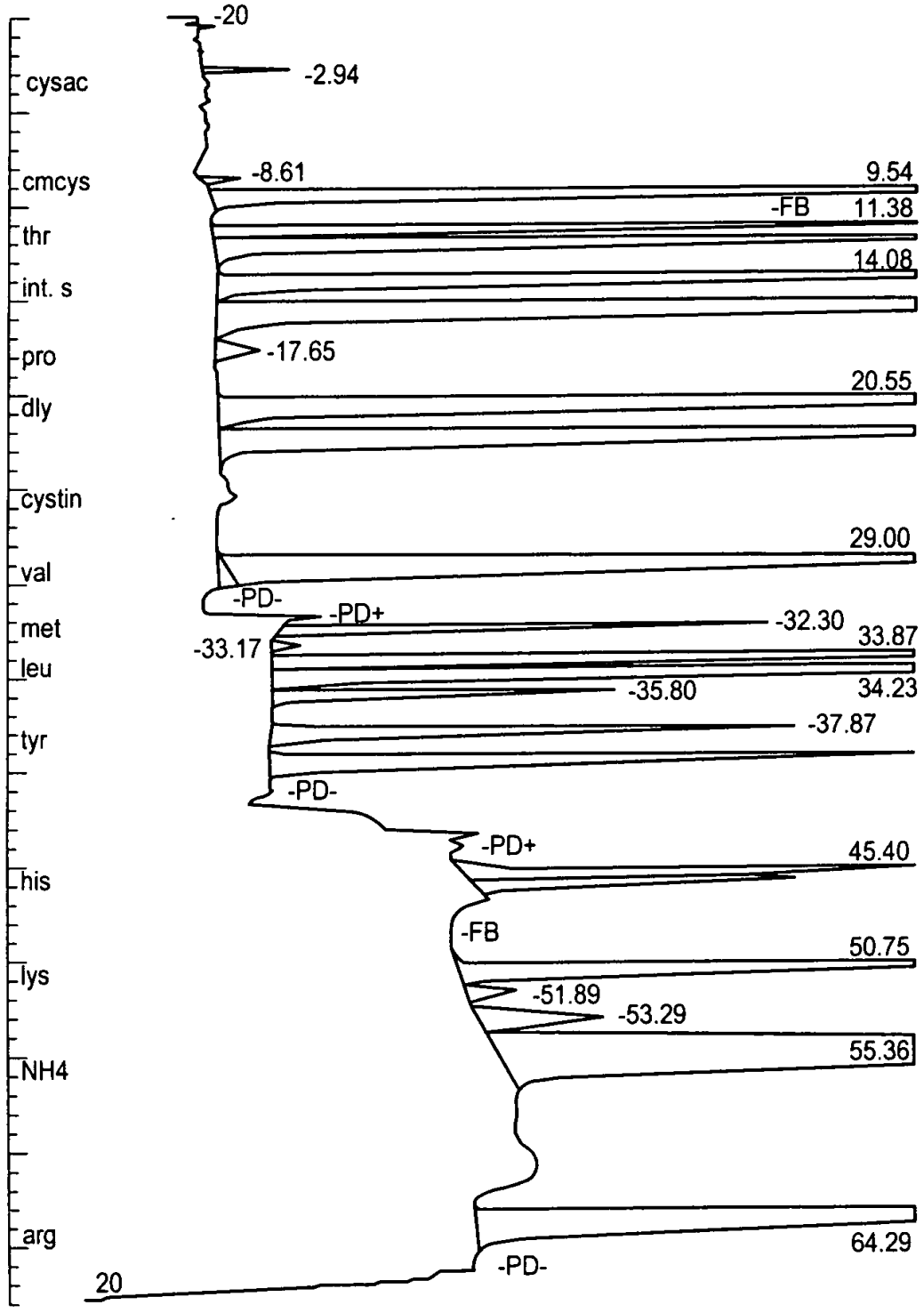


FIG. 5b

EXTERNAL STANDARD TABLE

********** 11-22-2000 14 : 28 : 43 Version 4.1 **********

Sample Name: amino acid analysis Data File: K:BAA936

Date: 11-22-2000 14 : 26 : 30 Method: F:REBECKA 11-22-2000 13 : 55 : 21 # 257

Interface: 0 Cycle #: 936 Operator jmc Channel #: 1 Vial #: N.A.

Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

****

Starting Delay: 0.00
Area reject: 5000
Amount injected: 1.00
Sample weight: 1.000000

Ending retention time: 68.00
One sample per: 2.002 sec.
Dilution factor: 1.00

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/ AREA
1	8.775		0.0000	0.0000%	5143	286	18.0	1			0.0000E+00
2	9.510		0.0000	0.0000%	129394	7707	16.8	1			0.0000E+00
3	11.345		0.0000	0.0000%	24969	1171	21.3	2			0.0000E+00
4	12.079		0.0000	0.0000%	59106	2389	24.7	2			0.0000E+00
5	14.047		0.0000	0.0000%	47121	1978	23.8	1		.2393	0.0000E+00
6	15.616	glx	6.2317	74.6757%	375516	13802	27.2	1	7	0	1.6595E-05
7	17.651	pro+cys	(2.1133)	25.3244%	199944	6665	30.0	1	7		1.0570E-05
8	20.554		0.0000	0.0000%	83682	2753	30.4	1			0.0000E+00
9	22.222		0.0000	0.0000%	67237	2027	33.2	1			0.0000E+00

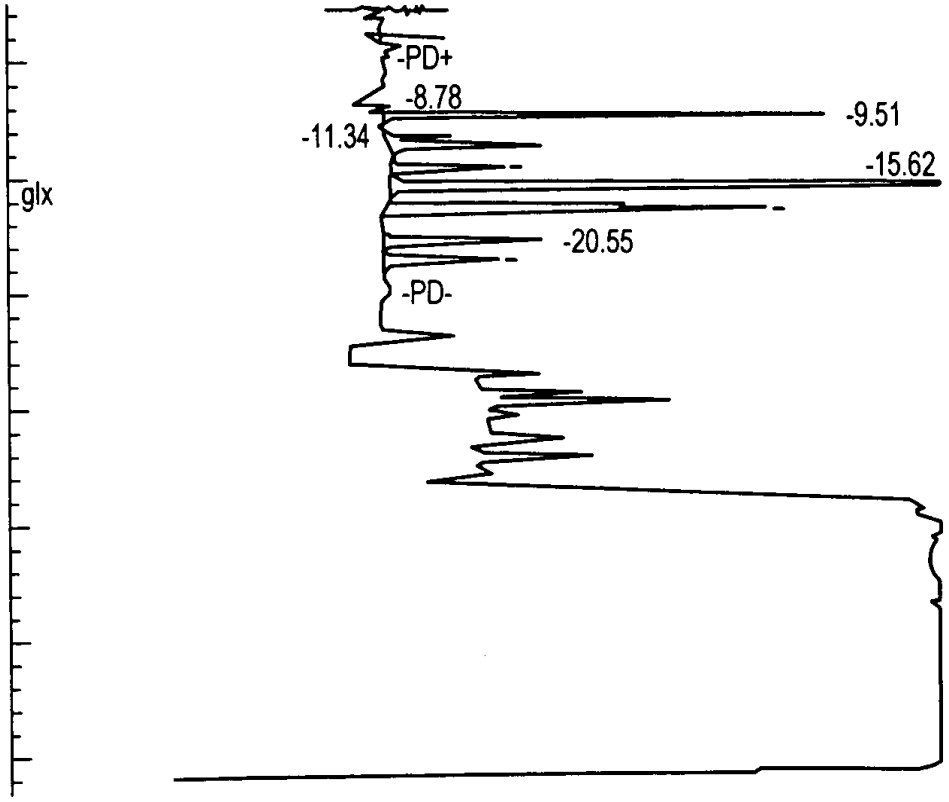
TOTAL AMOUNT: 8.3451

SEE FIG. 5c2

FIG. 5c1

SEE FIG. 5c1

AREAS, TIMES, AND HEIGHTS STORED IN : K: BAA936.ATB
DATA FILE = K: BAA936.PTS PRINTED ON 11-22-2000 AT 14:28:59
START TIME : 0.00 min. STOP TIME : 68.00 min. OFFSET : -95 mv
FULL RANGE : 15 millivolts



F I G. 5c2